

1600



PT/15 1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/619,310B

DATE: 10/31/2002
TIME: 16:05:24

Input Set : A:\3759-0106P.ST25.txt
Output Set: N:\CRF4\10312002\I619310B.raw

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ENTERED

3 <110> APPLICANT: THASTRUP, Ole
4 TULLIN, Soren
5 POULSEN, Lars K
6 BJORN, Sara P
8 <120> TITLE OF INVENTION: Novel Fluorescent Proteins
10 <130> FILE REFERENCE: 3759-0106P
12 <140> CURRENT APPLICATION NUMBER: 09/619,310B
13 <141> CURRENT FILING DATE: 2000-07-19
15 <150> PRIOR APPLICATION NUMBER: US 08/819,612
16 <151> PRIOR FILING DATE: 1997-03-17
18 <150> PRIOR APPLICATION NUMBER: PCT/DK96/00051
19 <151> PRIOR FILING DATE: 1996-01-31
21 <150> PRIOR APPLICATION NUMBER: DK 1065/95
22 <151> PRIOR FILING DATE: 1995-09-22
24 <160> NUMBER OF SEQ ID NOS: 23
26 <170> SOFTWARE: PatentIn version 3.1
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 36
30 <212> TYPE: DNA
31 <213> ORGANISM: Artificial Sequence
33 <220> FEATURE:
34 <223> OTHER INFORMATION: GFP2 primer directed to A. victoria
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40 <210> SEQ ID NO: 2
41 <211> LENGTH: 36
42 <212> TYPE: DNA
43 <213> ORGANISM: Artificial Sequence
45 <220> FEATURE:
46 <223> OTHER INFORMATION: GFP-1 primer directed to A. victoria
48 <400> SEQUENCE: 2
49 aagaattcgg atccctttag tgtcaattgg aagtct 36
52 <210> SEQ ID NO: 3
53 <211> LENGTH: 67
54 <212> TYPE: DNA
55 <213> ORGANISM: Artificial Sequence
57 <220> FEATURE:
58 <223> OTHER INFORMATION: 5' PCR primer incorporating the Y66H substitution responsible
for
59 changing green fluorescence into blue fluorescence
61 <400> SEQUENCE: 3
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64 gataccc 67
67 <210> SEQ ID NO: 4

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68 <211> LENGTH: 36
69 <212> TYPE: DNA
70 <213> ORGANISM: Artificial Sequence
72 <220> FEATURE:
73 <223> OTHER INFORMATION: 3' PCR primer incorporating the Y66H substitution responsible
for
74 changing green fluorescence into blue fluorescence
76 <400> SEQUENCE: 4
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81 <211> LENGTH: 30
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83 <213> ORGANISM: Artificial Sequence
85 <220> FEATURE:
86 <223> OTHER INFORMATION: 5' primer used to flank the Y66H-GFP
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89 aattggtacc aaggaggtaa gctttatgag 30
92 <210> SEQ ID NO: 6
93 <211> LENGTH: 30
94 <212> TYPE: DNA
95 <213> ORGANISM: Artificial Sequence
97 <220> FEATURE:
98 <223> OTHER INFORMATION: 3' primer used to flank the Y66H-GFP
100 <400> SEQUENCE: 6
101 ctttcgtttt gaattcggat cccttttagtg 30
104 <210> SEQ ID NO: 7
105 <211> LENGTH: 48
106 <212> TYPE: DNA
107 <213> ORGANISM: Artificial Sequence
109 <220> FEATURE:
110 <223> OTHER INFORMATION: large NcoI-XbaI vector fragment and ligated to SEQ ID NO:8
112 <400> SEQUENCE: 7
113 catggccaaac gcttgcact actctctt atgggttca atgctttt 48
116 <210> SEQ ID NO: 8
117 <211> LENGTH: 48
118 <212> TYPE: DNA
119 <213> ORGANISM: Artificial Sequence
121 <220> FEATURE:
122 <223> OTHER INFORMATION: synthetic NcoI-XbaI DNA linker and ligated to SEQ ID NO:7
124 <400> SEQUENCE: 8
125 ctagaaaagc attgaacacc ataagagaga gtatgtacaa gcgttggc 48
128 <210> SEQ ID NO: 9
129 <211> LENGTH: 48
130 <212> TYPE: DNA
131 <213> ORGANISM: Artificial Sequence
133 <220> FEATURE:
134 <223> OTHER INFORMATION: large NcoI-XbaI vector fragment ligated to SEQ ID NO:10
136 <400> SEQUENCE: 9
137 catggccaaac gcttgcact actctcactt atgggttca atgctttt 48
140 <210> SEQ ID NO: 10

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141 <211> LENGTH: 48
 142 <212> TYPE: DNA
 143 <213> ORGANISM: Artificial Sequence
 145 <220> FEATURE:
 146 <223> OTHER INFORMATION: Ncol-Xba1 DNA linker ligated to SEQ ID NO:9
 148 <400> SEQUENCE: 10
 149 cttagaaaagc attgaacacc ataagtgaga gtagtgacaa gcgttggc 48
 152 <210> SEQ ID NO: 11
 153 <211> LENGTH: 36
 154 <212> TYPE: DNA
 155 <213> ORGANISM: Artificial Sequence
 157 <220> FEATURE:
 158 <223> OTHER INFORMATION: 5' primer based on pGFP-N1 plasmid
 160 <400> SEQUENCE: 11
 161 tggaaaataagc tttatgatgta aaggagaaga actttt 36
 164 <210> SEQ ID NO: 12
 165 <211> LENGTH: 35
 166 <212> TYPE: DNA
 167 <213> ORGANISM: Artificial Sequence
 169 <220> FEATURE:
 170 <223> OTHER INFORMATION: 3' primer based on pGFP-N1 plasmid
 172 <400> SEQUENCE: 12
 173 gaatcgtaga tctttatggat tatagttcat ccatg 35
 176 <210> SEQ ID NO: 13
 177 <211> LENGTH: 40
 178 <212> TYPE: DNA
 179 <213> ORGANISM: Artificial Sequence
 181 <220> FEATURE:
 182 <223> OTHER INFORMATION: 5' primer based on pZeoSV-LacZ plasmid
 184 <400> SEQUENCE: 13
 185 tggaaaataagc tttatggatcccgatcgatccatgac 40
 188 <210> SEQ ID NO: 14
 189 <211> LENGTH: 34
 190 <212> TYPE: DNA
 191 <213> ORGANISM: Artificial Sequence
 193 <220> FEATURE:
 194 <223> OTHER INFORMATION: 3' primer based on pZeoSV-LacZ plasmid
 196 <400> SEQUENCE: 14
 197 ggcgcgaattc ttattattat ttttgacacc agac 34
 200 <210> SEQ ID NO: 15
 201 <211> LENGTH: 764
 202 <212> TYPE: DNA
 203 <213> ORGANISM: Aequorea Victoria
 205 <220> FEATURE:
 206 <221> NAME/KEY: CDS
 207 <222> LOCATION: (8)..(721)
 208 <223> OTHER INFORMATION:
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 212 aagcttt atg agt aaa gga gaa gaa ctt ttc act gga gtt gtc cca att 49

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213	Met	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile			
214	1			5					10								
216	ctt	gtt	gaa	tta	gat	ggc	gat	gtt	aat	ggg	caa	aaa	ttc	tct	gtt	agt	97
217	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	Gln	Lys	Phe	Ser	Val	Ser	
218	15				20				25			30					
220	gga	gag	ggt	gaa	ggt	gat	gca	aca	tac	gga	aaa	ctt	acc	ctt	aaa	ttt	145
221	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	
222												35		40		45	
224	att	tgc	act	act	ggg	aag	cta	cct	gtt	cca	tgg	cca	acg	ctt	gtc	act	193
225	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	
226										50		55		60			
228	act	ttc	tct	tat	ggt	gtt	caa	tgc	ttt	tca	aga	tac	cca	gat	cat	atg	241
229	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	
230							65			70		75					
232	aaa	cag	cat	gac	ttt	ttc	aag	agt	gcc	atg	ccc	gaa	ggt	tat	gta	cag	289
233	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	
234							80			85		90					
236	gaa	aga	act	ata	ttt	tac	aaa	gat	gac	ggg	aac	tac	aag	aca	cgt	gct	337
237	Glu	Arg	Thr	Ile	Phe	Tyr	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	
238	95					100				105			110				
240	gaa	gtc	aag	ttt	gaa	ggt	gat	acc	ctt	gtt	aat	aga	atc	gag	tta	aaa	385
241	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	
242							115			120			125				
244	ggt	att	gat	ttt	aaa	gaa	gat	gga	aac	att	ctt	gga	cac	aaa	atg	gaa	433
245	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Met	Glu	
246							130			135			140				
248	tac	aac	tat	aac	tca	cat	aat	gta	tac	atc	atg	gca	gac	aaa	cca	aag	481
249	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Pro	Lys	
250							145			150			155				
252	aat	gga	atc	aaa	gtt	aac	ttc	aaa	att	aga	cac	aac	att	aaa	gat	gga	529
253	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Lys	Asp	Gly	
254							160			165			170				
256	agc	gtt	caa	tta	gca	gac	cat	tat	caa	caa	aat	act	cca	att	ggc	gat	577
257	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	
258	175					180				185			190				
260	ggc	cct	gtc	ctt	tta	cca	gac	aac	cat	tac	ctg	tcc	acg	caa	tct	gcc	625
261	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	
262							195			200			205				
264	ctt	tcc	aaa	gat	ccc	aac	gaa	aag	aga	gat	cac	atg	atc	ctt	ctt	gag	673
265	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Ile	Leu	Glu		
266							210			215			220				
268	ttt	gta	aca	gct	gct	ggg	att	aca	cat	ggc	atg	gat	gaa	cta	tac	aaa	721
269	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	Leu	Tyr	Lys	
270							225			230			235				
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276	<211>	LENGTH:	238														
277	<212>	TYPE:	PRT														
278	<213>	ORGANISM:	Aequorea Victoria														

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280 <400> SEQUENCE: 16
 282 Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 283 1 5 10 15
 286 Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser Gly Glu
 287 20 25 30
 290 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 291 35 40 45
 294 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 295 50 55 60
 298 Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
 299 65 70 75 80
 302 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 303 85 90 95
 306 Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 307 100 105 110
 310 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 311 115 120 125
 314 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn
 315 130 135 140
 318 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly
 319 145 150 155 160
 322 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly Ser Val
 323 165 170 175
 326 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 327 180 185 190
 330 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
 331 195 200 205
 334 Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu Phe Val
 335 210 215 220
 338 Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
 339 225 230 235
 342 <210> SEQ ID NO: 17
 343 <211> LENGTH: 764
 344 <212> TYPE: DNA
 345 <213> ORGANISM: Aequorea victoria
 347 <220> FEATURE:
 348 <221> NAME/KEY: CDS
 349 <222> LOCATION: (8)..(724)
 350 <223> OTHER INFORMATION:

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354 aagcttt atg agt aaa gga gaa gaa ctt ttc act gga gtt gtc cca att 49
 355 Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile
 356 1 5 10
 358 ctt gtt gaa tta gat ggc gat gtt aat ggg caa aaa ttc tcc gtt agt 97
 359 Leu Val Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser
 360 15 20 25 30
 362 gga gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt 145
 363 Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
 364 35 40 45

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L:353 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:17,Line#:350
L:495 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:19,Line#:492
L:651 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:21,Line#:648